

Amendments to the Specification:

Please replace the paragraph beginning on page 3 line 29 and continuing through page 4 line 11 with the following replacement paragraph (amendment filed on May 12, 2006 is reflected below):

Figures 1A, B, C, D, E, F, and G through 1J show an alignment of AXMI-014 (SEQ ID NO:3) with cry1Aa (SEQ ID NO:6), cry1Ac (SEQ ID NO:7), cry1Ia (SEQ ID NO:8), cry2Aa (SEQ ID NO:9), cry3Aa1 (SEQ ID NO:10), cry3Bb (SEQ ID NO:11), cry4Aa (SEQ ID NO:12), cry4Ba (SEQ ID NO:13), cry6Aa (SEQ ID NO:14), cry7Aa (SEQ ID NO:15), cry8Aa (SEQ ID NO:16), cry10Aa (SEQ ID NO:17), cry16Aa (SEQ ID NO:18), cry19Ba (SEQ ID NO:19), cry24Aa (SEQ ID NO:20), cry25Aa (SEQ ID NO:21), cry39Aa1 (SEQ ID NO:22), and cry40Aa1 (SEQ ID NO:23). Toxins having C-terminal non-toxic domains were artificially truncated as shown. Conserved group 1 is found from about amino acid residue 180 to about 201 of SEQ ID NO:3. Conserved group 2 is found from about amino acid residue 261 to about 303 of SEQ ID NO:3. Conserved group 3 is found from about amino acid residue 486 to about 536 of SEQ ID NO:3. Conserved group 4 is found from about amino acid residue 554 to about 564 of SEQ ID NO:3.

Please replace the paragraph beginning on page 12 line 29 and continuing through page 13 line 9 with the following replacement paragraph:

Amino acid substitutions may be made in nonconserved regions that retain function. In general, such substitutions would not be made for conserved amino acid residues, or for amino acid residues residing within a conserved motif, where such residues are essential for protein activity. Examples of residues that are conserved and that may be essential for protein activity include, for example, residues that are identical between all proteins contained in the alignment of Figures 1A, B, C, D, E, F, and G through 1J. Examples of residues that are conserved but that may allow conservative amino acid substitutions and still retain activity include, for example, residues that have only conservative substitutions between all proteins contained in the alignment of Figures 1A, B, C, D, E, F, and G through 1J. However, one of skill in the art would understand that functional variants may have minor conserved or nonconserved alterations in the conserved residues.

Please replace lines 3-7 on page 35 with the following replacement paragraph:

Analysis of the DNA sequence of pAX014 by methods known in the art identified an open reading frame with homology to known delta endotoxin genes. This open reading frame is designated as AXMI-014. The DNA sequence of AXMI-014 is provided as SEQ ID NO:1, and the amino acid sequence of the predicted AMXI-008 protein is provided as SEQ ID NO:[2]3. An alternate start site for AXMI-014 at nucleotide 136 of SEQ ID NO:1 generates the amino acid sequence provided as SEQ ID NO:5.